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Details

Range: from to

☐ Reverse complemented strand

Features:

☐ SNP

☐ CDD

☒ MGC

☐ 1: [BC033025](#). Reports Homo sapiens HTPA...[gi:21542540]

Links

LOCUS BC033025 2204 bp mRNA linear PRI 06-OCT-2003

DEFINITION Homo sapiens HTPAP protein, mRNA (cdna clone MGC:32924

IMAGE:5267610), complete cds.

ACCESSION BC033025

VERSION BC033025.1 GI:21542540

KEYWORDS MGC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2204)

AUTHORS

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

TITLE
Schnersch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE
22388257

PUBMED
12477932

REFERENCE
2 (bases 1 to 2204)

AUTHORS
Strausberg, R.

TITLE
Direct Submission

JOURNAL
Submitted (21-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbiology.org>
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 47 Row: 1 Column: 8
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 14210481.
Differences found between this sequence and the human genome (build
35) are described in misc_difference features below and these
differences were also compared to chimpanzee genomic sequences
available as of Sep 03, 03.

FEATURES
source
1..2204
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:32924 IMAGE:5267610"
/tissue_type="Testis"

```

/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/note="Vector: pBluescript"
1..2204
/gene="HTPAP"
/db_xref="LocusID:84513"
misc_difference 1
/gene="HTPAP"
/note="1 base at the 5' end does not align to the human
genome."
misc_difference 5
/gene="HTPAP"
/note="'G' in cDNA is 'C' in the human genome. The
chimpanzee genome agrees with the cDNA sequence,
suggesting that this difference is unlikely to be due to
an artifact."
misc_difference 5^6
/gene="HTPAP"
/note="1 base in the human genome, T, is not found in
cDNA. The chimpanzee genome agrees with the cDNA
sequence, suggesting that this difference is unlikely to
be due to an artifact."
205..876
CDS
/gene="HTPAP"
/codon_start=1
/product="HTPAP protein"
/protein_id="AAH33025.1"
/db_xref="GI:21542541"
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GRKSFPSGHSSFAFAGLAFASFYLAGKLHCFTPPQGRGKSWRFAFLSPLLFAAVIALS
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YCFDI"
misc_feature 379..786
/gene="HTPAP"
/note="PAP2; Region: PAP2 superfamily. This family
includes the enzyme type 2 phosphatidic acid phosphatase
(PAP2), Glucose-6-phosphatase EC:3.1.3.9,
Phosphatidylglycerophosphatase B EC:3.1.3.27 and bacterial
acid phosphatase EC:3.1.3.2"
/db_xref="CDD:pfam01569"

```

misc difference 1169..1170
/gene="HTPAP"
/note="2 bases in cDNA are not found in the human genome.
The chimpanzee genome agrees with the cDNA sequence,
suggesting that this difference is unlikely to be due to
an artifact."
misc difference 2188..2204
/gene="HTPAP"
/note="polyA tail: 17 bases do not align to the human
genome."

ORIGIN

```
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61  ccaggcaggc gggcggcacg gggcgcgagg tgggcagtg ggaagcggg gaggaagcca
121 ggcgacctgc tctgcgcttc ttgttcccc tctagggtga cggagctgct ccccccttc
181 cagagactca tccagccgga ggagatggg cttaccgga accctacgt ggagcggag
241 tatttcccc ccaagccgat gttgttatt gcatttctct ctccactgtc tctgatcttc
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481 tgtacagggg ataaggacct ggtgaatgag ggcgaaaga gctccccag tggacattct
541 tcccttgcat ttgctggctt ggcctttgog tcccttacc tggcagggaa gttacactgc
601 ttcacaccac aaggccgtgg gaaatcttgg aggttctgtg ccttctgtc acctctactt
661 tttagcagtg tgattgcact gtcccgcaca tgtgactaca agcatcactg gcaagatgta
721 ctagtgtgat ccattgattg aatgacattt gcctatgtct gctatcggca gtattatcct
781 cctctgactg atgcagaatg ccataaacca ttccaagaca aacttgtact ttccactgca
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901 ggctcatgcc tghtaatcca acactttggg aggtcaggga ggttgatcca cctgaggtca
961 ggaccagcct ggccaacatg gtgaaccctg tctctactaa aaatacaaaa attagccagg
1021 agtttgtgtc cgtaatccca gctacctggg aggtcagggt aggagaattg cttgaacctg
1081 ggagctggag gttccagtga gccgagatcg caccactgca tccagccta ggcaacagag
1141 tgagacccca tctcaaaaaa aaaaaaaaaa ttgaatctat ctcaatagag aacaggtgaa
1201 ctagccctcc taaccggacc atgcacaaga caagaaattc tagccttttt ttcccccttc
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1441 atctgaagat ctacagtgtt ttacatttta atttaaatgc cattcttaga aggatcttgt
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1561 ttaatttcca ttcatatag ctcaaaatct taaaatctag ggcattggcca actaaattac
1621 tttagattctg ttacaccttc ctgatgacaa ttccatcaag ccttaaatag gaaaatgtcg
1681 aatctagggt aatttatcac ttttgtgtgc atcttatctg agtccagcca tctggtactg
1741 ctgtgcattt tgaacaccgt gggcataaac aatttgttga attactaagt gaaaacaata
1801 ataaagaaga aaatggtcag gagtgtggtt tcagcactac taacagatga ctgtttctac
```

1861 ctcaatttgac cataactgtg cttgtgagct tttttccttc cattcatgac tgaagatctg
1921 ctcaaatgca ccaacactgc caagtgacta aggtagaataa gaaaaatgac aggtatcgtc
1981 atctgaagga cagatgaatc tttttctgcc ccttcttcac aatggaatat aggaacaat
2041 tatgggatgt catcagaatg gatgccatag gacctacagc tccctttctc tttattgtga
2101 ttatacttta aatatgacat tgccttttat gtgtatgttc ctatattttc aatgtatctt
2161 tttccttcag taaacctgat attcaaacaa aaaaaaaaaa aaa

//

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Dec 8 2004 11:02:33



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Books

Sequence Revision History

Find (Accessions, GI numbers or Fasta style SeqIds) **BC033025**

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Gi Version

Update Date

21542540

1

Oct 6 2003 7:25 PM

21542540

1

Jun 24 2002 4:50 PM

Search for Genes

LocusLink provides curated information for human, fruit fly, mouse, rat, and zebrafish

Accession = BC033025, Locus = BC033025

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Check sequence revision history

How to create WWW links to Entrez

LinkOut

Cubby

Related resources

BLAST

Reference sequence project

LocusLink

Differences in LOCUS names:

old: "LOCUS BC033025
24-JUN-2002"

new: "LOCUS BC033025
06-OCT-2003"

2204 bp mRNA linear PRI

2204 bp mRNA linear PRI

Differences in DEFINITION:

old: "Homo sapiens, Similar to HTPAP protein, clone MGC:32924 IMAGE:5267610,
mRNA, complete cds."

new: "Homo sapiens HTPAP protein, mRNA (cDNA clone MGC:32924 IMAGE:5267610),
complete cds."

Differences in REFERENCE:

Changed reference:

refline:

old: "1 (bases 1 to 2204)"

new: "2 (bases 1 to 2204)"

New reference:

Clusters of orthologous groups

Protein reviews on the web

refline: "1 (bases 1 to 2204)"
 authors: "Strausberg,R.L., Feingold,E.A., Grouse,L.H.,
 Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L.,
 Shenmen,C.M., Schuler,G.D., Altschul,S.F.,
 Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
 Hopkins,R.F., Jordan,H., Moore,T., Max,S.I.,
 Wang,J., Hsieh,F., Diatchenko,L., Marusina,K.,
 Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M.,
 Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
 Scheetz,T.E., Brownstein,M.J., Usdin,T.B.,
 Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S.,
 Loquellano,N.A., Peters,G.J., Abramson,R.D.,
 Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
 McKernan,K.J., Malek,J.A., Gunaratne,P.H.,
 Richards,S., Worley,K.C., Hale,S., Garcia,A.M.,
 Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M.,
 Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J.,
 Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
 Sanchez,A., Whiting,M., Madan,A., Young,A.C.,
 Shevchenko,Y., Bouffard,G.G., Blakesley,R.W.,
 Touchman,J.W., Green,E.D., Dickson,M.C.,
 Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
 Butterfield,Y.S., Krzywinski,M.I., Skalska,U.,
 Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J.
 and Marra,M.A."
 title: "Generation and initial analysis of more than 15,000
 full-length human and mouse cDNA sequences"
 journal: "Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903
 (2002)"
 muid: "22388257"
 pmid: "12477932"

Differences in FEATURE.CDS:

```

-----
Changed feature CDS 205..876
Changed /product =
old: "Similar to HTPAP protein"
      ^
new: "HTPAP protein"
      ^
New /db_xref = "LocusID:84513"
New /gene = "HTPAP"
```

Differences in FEATURE.gene:

```
-----  
New feature      gene      1..2204  
                  /db_xref  = "LocusID:84513"  
                  /gene     = "HTPAP"
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Differences in FEATURE.misc_feature:

```
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New feature      misc_feature  379..786  
                  /db_xref    = "CDD:pfam01569"  
                  /gene       = "HTPAP"  
                  /note       = "PAP2; Region: PAP2 superfamily. This  
                                family includes the enzyme type 2  
                                phosphatidic acid phosphatase (PAP2),  
                                Glucose-6-phosphatase EC:3.1.3.9,  
                                Phosphatidylglycerophosphatase B  
                                EC:3.1.3.27 and bacterial acid phosphatase  
                                EC:3.1.3.2"
```

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